

# Resource Summary Report

Generated by [dkNET](#) on Aug 31, 2026

## DISENTANGLER

RRID:SCR\_009161

Type: Tool

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### Proper Citation

DISENTANGLER (RRID:SCR\_009161)

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### Resource Information

**URL:** <http://kumasakanatsuhiko.jp/projects/disentangler/>

**Proper Citation:** DISENTANGLER (RRID:SCR\_009161)

**Description:** Software application that is a visualization technique for linkage disequilibrium mapping and haplotype analysis of multiple multi-allelic genetic markers. (entry from Genetic Analysis Software)

**Abbreviations:** DISENTANGLER

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic, java/jre1.5, bio.tools

**Resource Name:** DISENTANGLER

**Resource ID:** SCR\_009161

**Alternate IDs:** nlx\_154284, blotools:disentangler

**Alternate URLs:** <https://bio.tools/disentangler>

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260829T183054+0000

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### Ratings and Alerts

No rating or validation information has been found for DISENTANGLER.

No alerts have been found for DISENTANGLER.

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### Data and Source Information

## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

Kang B, et al. (2026) Recurrent connections facilitate occluded object recognition by explaining-away. Nature communications, 17(1).

Morita M, et al. (2026) Long-read KIR genotyping reveals donor KIR/HLA polymorphisms linked to posttransplant relapse in T-cell malignancies. Blood advances, 10(13), 4563.

Liu Z, et al. (2024) Human leukocyte antigen-DQA1\*04:01 and rs2040406 variants are associated with elevated risk of childhood Burkitt lymphoma. Communications biology, 7(1), 41.

Valenzuela-Ponce H, et al. (2023) Honduras HIV cohort: HLA class I and CCR5-??32 profiles and their associations with HIV disease outcome. Microbiology spectrum, 11(6), e0161323.

Dallmann-Sauer M, et al. (2020) The complex pattern of genetic associations of leprosy with HLA class I and class II alleles can be reduced to four amino acid positions. PLoS pathogens, 16(8), e1008818.

Ferreiro-Iglesias A, et al. (2018) Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature communications, 9(1), 3927.